

31 ATGGCAACAGCTGAGGAATCGAACGCCATCGAATGGCCACCGCCACAGTACGCTCCTGGAAGGAGCTGTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
 91 GAGGAGCGCCGACTGGAGCCCAAGCGAGCAAAACAGAGCCATAGAACCAAGCCCATCTCGGCCACCTGAGCCAACTGAGCCACCTG
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
 181 CTCATCATCGCGGACTGTGATCGTCTGTGTGGCGGCGGTGACGGAGGCGCGCGGCATGGCCGCTCATGTTCGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
 271 GGCAGGCGGTCCAACCGACCGGTCAACCGAATGCCAGTTTGGCAAGTTTGGCGGAATTGGGTCCACCTGGTATGCGGATTTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
 361 CCACCTTCGGAGTTATGTAATCAAGTGTGAATGTGCGCATACCAAGAGCGGCGCATCGTTGCACGCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K R R I V A R V Q C R N
 451 ATCAAAAACGAGTGGCGCGGCGCAAAATGCGATGATCCCATCTCGTTGGCGGAAATGCTGCAAGACCTGTCCCGCGGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
 541 ACGATGTAGCCTTGGATGTGCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAACAATTACGCTGCGTTGCTAACGGGCGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 631 TATTTCTCAAGGTGAGGAATGAAGTCCATGTACACACCTACAATCGGAGAAATCTGGTGGCCACCGCCCGTTTCTGTTCACCAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
 721 AAGAATCTATCTACTCTTCTACACCTCATCGGAATCGGTGCGGTGCGCATTCATTCGTTGATGATCGGGGTGTAATCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
 811 GAGCATCAACTGGAGACCACTTGGCGGCGACTCTCAGTGTCTATCAGAATGCCACGGCAAGATCTGA
 271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

FIGURE 1

1 ATGGCCACAAGCTGAGGAATCGAAGCCCATCGAATGGGCCACGCCACCGGCACAGTACCGCTCTCTGGAAGAGCTGCTGCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
91 GAGGACGCCGACTGGAGCCCCAAGCAGCAAAACACGACCATAGAGAACAGCCCCCATCTCGGCCACCTGAGCCACCTG
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
181 CTATCATCGCGGACTGCTGATCGTCTGTGGCGGCGTACGAGGGCGCGGCATGCGCGCTCATGTCGAGGAGTCCGACACG
61 L I I A G L L I V C L A G V T E G R R H A P L M F E S D T
271 GCGAGCGGTCCAACGACGACGCGGTCAACGAATGCCAGTTTGGCAAGTTTGGGTCCACCTGGTATGCGGATTTGGGT
91 G R S N R P A V T E C Q F G K V L R E L G S T M Y A D L G
361 CCACCCTTCGAGTTATGTACTGCATCAAGTGTGAATGTGCGCATACCCAAGAGCGCGCATCGTTGCACGCGTCCAGTGTCCGAAT
121 P P F G V M Y C I K C E C V A I P K R R I V A R V Q C R N
451 ATCAAAACGAGTCCCGCGGCAAAATGCGATGATCCCTCTGTTGCCGGAATGTGCAAGACCTGTCGCGCATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
541 ACGGATGTAGCTTGGATGTGCCCGTCCCAATGAAGAGGAGCGCAACATGAACATTACGTCGCTTGTACGGGCGCGCACCTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S
631 TATTTCTCAAGGTGAGGAATGAAGTCCATGTACACCACTACAATCCGAGAACTCTGTGGCCACCGCCCGTTTCTGTTCCACAAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
721 AAGAATCTACTCTTCTACACCTCATCGCAATCGTCTCGCGTCCCATTCATTCTGTTGATGATCGGGTGTAAATCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
811 GAGCATCAACTGGAGACCACTTGGCGGCACTCTCAGTGTCTATCAGATGCCAGGCAAGATCGGCGCGGTCCGAGGTACTCTTA
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L
901 GAGGATCTTCTGAAGGACCTTACTTCTGTCGTGTGACATAATGGACAAACTACCTACAGAGATTTAAAGCTCTAA
301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

TM

CRI

pLIAS
Sequences

FIGURE 2

1 ATGCCAACAAAGCTGAGGAAATCGAAATGGGCCACGGCCACGGCACAGTACCGCTCTGGAAGAGAGCTCTGCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
91 GAGGACGGCGCACTGGAGCCCCAAGCGAGCAAAACAGCATAGAGAAACAAGCCCCATCTGCGCCACTGAGCCAACTGAGCCACCTG
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
181 CTGATCGCGGACTGCTGATGCTGCTTGGCGGGGTGAGGAGGGCGCGGCATGCGCGCTCATGTTGAGGAGTCCGACACG
61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
271 GGCAGGCGGTCCAAACCGACCGGTACCGAATGCCAGTTTGGCAAAGTTTTGCGGAATGCGGTCCACCTGGTATGCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
361 CCACCTTCGGAGTTATGCTACTGTCATCAAGTGTGAATGTGTGCGCATACCCAAAGAGCGGGCGCATCGTTGCACGCTCCAGTGTGCAAT
121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N
451 ATGAAAACGAGTCCCGCGGCAAAATGCGATCCCATCTGTTGCCGGAATAATGCTGCAAGACTGTGCCGGGATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
541 ACGGATGTAGCCTTGGATGTGCCCGTCCCAATGAAGAGGAAGAGCGCAACATGAACATTTAGCTGCGTTGCTAACGGGCGGCACCTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S
631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACTTACAATCCGCAAGATCTGTGTGGCCACCGCGTTTCTGTTCCACAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
721 AAGAATCTATACTCTTACACCTCATCGGGAATCGGTGCTCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAACTCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
811 GAGCATCAACTGGAGACCACCTTGGCGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGCCGGCTCGAGGTACCTCTA
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L
901 GAGGATCTTTGTGAAGAACCTTACTTCTGTGGTGTGACATAAATGGACAAACTACTACAGAGATTTAAAGCTCTAA
301 E D L C E G T L L L L W C D I I G N T T Y R D L K L STOP

TM
CRI:W->A
pUAS
Sequences

FIGURE 3

1 ATGCCAACAAAGCTGAGGAAATCGAACGCCATCGAATGGGCACGGCCACGGCACAGTACCGCTCTCTGGAAGGAGCTGCTCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACTGGAGCCCCAAGCAGAGCAAAAACGAGCCATAGAGAAACAGCCCATCTGCGCACCTGAGCCAACTGAGCCACCTG TM
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATCGCCGGAAGTCTGCTGCTGGCGGGGTGACGGAGGGCGCGCGCATGRRHAPLMFEESDT
61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GCGAGCGGTCCAACCGACGAGCGGTACCGAATGCCAGTTTGGCAAGTTTGGCGAATTGGGTCCACCTGGTATCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCAAGAGCGCGCATCGTTGCACGCGTCCAGTGTGCGCAAT CRI
121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAACGAGTGCCTGGCGGCAAAATGCGATGATCCCATCTCTGTGCGGAAATGTGCAAGACCTGTCCCGCGCATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTTGGATGTGCCGTGCCCAATGAGAGGAAGCGGCAACATGAAACATTACGCTGCGTTGCTAACGGGCGCACCTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGTTGAGGAAATGAAGTCCATGTACACCACTACAATCGCAGAAATCTGGTGGCCACCGCGCTTCTCTGTTCCACAAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTGCTCGGTGCCATTCAATTCTGTTGATGCGGGTGTAAATCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACTTGGCGGCACTCTCAGTCTCTATCAGAAATGCCAGGCAAGATCGGCGGGCTCGAGGCGAGCGCGG
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R N R G PUAS/PCR

901 CGCATCTTTTACCCATACGATGTTCTGACTATGGGGTATCCCTATCAGTCCCGGACTATGACGATCTTATCCATATGACCTTCCA
301 R I F Y P Y D V F D Y A G Y P Y D V P D Y A G S Y P Y D V P SX-HA

991 GATTACGCTGCTCAGTGGCGCGATTATACGGAGCAGCGACAAATCA
331 D Y A A N C G R D Y K D D D K stop IX-FLAG

FIGURE 4

	10	20	30	40	50	60	70
Nog protei	MDHSQCLVTIYALMWFLGLRIDGGCGHYLHIRPASENLPVLDLIEHPDPIYDPKEKDLNETLLRTLMVGHFDP						
SuperSog P [71]	<hr/>						
	260	270	280				
	iqfvddagvile--EhqletTLaGTLSv--ygn						
	^^^^^^^vv^ ^-^-^-^VV^v^ ^v						
Nog protei	VDLIEHPDPIYDPKEKDLNETLLRTLMVGHFDP						

[illegible]

Nog protei

FIGURE 5

[illegible]